



IFWO

RAW SEQUENCE LISTING DATE: 09/01/2004
PATENT APPLICATION: US/10/825,898 TIME: 13:06:27

Input Set : N:\Crdf3\RULE60\10825898.raw
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1 <110> APPLICANT: BOYLE, WILLIAM
 2 <120> TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
 3 <130> FILE REFERENCE: A-451K REV 09-10-03 54SEQ
 C--> 4 <140> CURRENT APPLICATION NUMBER: US/10/825,898
 C--> 5 <141> CURRENT FILING DATE: 2004-04-15
 6 <150> PRIOR APPLICATION NUMBER: US/10/825,898
 7 <151> PRIOR FILING DATE: 2004-04-15
 8 <150> PRIOR APPLICATION NUMBER: US 09/052,521
 9 <151> PRIOR FILING DATE: 1998-03-30
 10 <150> PRIOR APPLICATION NUMBER: US 08/880,855
 11 <151> PRIOR FILING DATE: 1997-06-23
 12 <150> PRIOR APPLICATION NUMBER: US 08/842,842
 13 <151> PRIOR FILING DATE: 1997-04-16
 14 <160> NUMBER OF SEQ ID NOS: 54
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2295
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Mus musculus
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (158)..(1105)
 24 <223> OTHER INFORMATION:
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27	cggggggccgc ctggccggga gtctgctcgg cgggtgggtgg ccgaggaagg gagagaacga	120
28	tgcggagca gggcgccccga actccggcgcc ccgcgc atg cgc cgg gcc agc cga	175
29	Met Arg Arg Ala Ser Arg	
30	1 5	
31	gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc agc ggc ccc	223
32	Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro	
33	10 15 20	
34	ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct gca ccg gct	271
35	Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala	
36	25 30 35	
37	ccg gcg cca ccc gcc tcc cgc tcc atg ttc ctg gcc ctc ctg	319
38	Pro Ala Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu	
39	40 45 50	
40	ggg ctg gga ctg ggc cag gtg gtc tgc agc atc gct ctg ttc ctg tac	367
41	Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr	
42	55 60 65 70	
43	ttt cga gcg cag atg gat cct aac aga ata tca gaa gac agc act cac	415
44	Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His	

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45	75	80	85	
46	tgc ttt tat aga atc ctc cat gaa aac gca ggt ttg cag gac			463
47	Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp			
48	90	95	100	
49	tcg act ctg gag agt gaa gac aca cta cct gac tcc tgc agg agg atg			511
50	Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met			
51	105	110	115	
52	aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa cac att gtg			559
53	Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val			
54	120	125	130	
55	ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa ggc tca tgg			607
56	Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp			
57	135	140	145	150
58	ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca ttt gca cac			655
59	Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His			
60	155	160	165	
61	ctc acc atc aat gct gcc agc atc cca tcg ggt tcc cat aaa gtc act			703
62	Leu Thr Ile Asn Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr			
63	170	175	180	
64	ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc tct aac atg			751
65	Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met			
66	185	190	195	
67	acg tta agc aac gga aaa cta agg gtt aac caa gat ggc ttc tat tac			799
68	Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr			
69	200	205	210	
70	ctg tac gcc aac att tgc ttt cgg cat cat gaa aca tcg gga agc gta			847
71	Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val			
72	215	220	225	230
73	cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa acc agc atc			895
74	Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile			
75	235	240	245	
76	aaa atc cca agt tct cat aac ctg atg aaa gga ggg agc acg aaa aac			943
77	Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn			
78	250	255	260	
79	tgg tcg ggc aat tct gaa ttc cac ttt tat tcc ata aat gtt ggg gga			991
80	Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly			
81	265	270	275	
82	ttt ttc aag ctc cga gct ggt gaa gaa att agc att cag gtg tcc aac			1039
83	Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn			
84	280	285	290	
85	cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt ggg gct ttc			1087
86	Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe			
87	295	300	305	310
88	aaa gtt cag gac ata gac tgagactcat ttctgtggAAC attagcatgg			1135
89	Lys Val Gln Asp Ile Asp			
90	315			
91	atgtccataga tgTTTggAAA cttcttaaaa aatggatgat gtctatacat gtgtaaGACT			1195
92	actaAGAGAC atggcccACG gtgtatgAAA ctcacAGCCC tctctttGA gcctgtACAG			1255
93	gttgtgtATA tgtaAAgtCC ataggTGTATG TTAGATTCA ggtgattaca caacggTTT			1315

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144	210	215	220
145	Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr		
146	225	230	235
147	Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys		240
148	245	250	255
149	Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr		
150	260	265	270
151	Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile		
152	275	280	285
153	Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala		
154	290	295	300
155	Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp		
156	305	310	315

158 <210> SEQ ID NO: 3

159 <211> LENGTH: 2271

160 <212> TYPE: DNA

161 <213> ORGANISM: Homo sapiens

162 <220> FEATURE:

163 <221> NAME/KEY: CDS

164 <222> LOCATION: (185)..(1135)

165 <223> OTHER INFORMATION:

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169	cgcagacaag aagggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag	180
170	cggcc atg cgc ggc agc aga gac tac acc aag tac ctg cgt ggc tcg	229
171	Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser	
172	1 5 10 15	
173	gag gag atg ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac	277
174	Glu Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His	
175	20 25 30	
176	gcc ccg ccg cct gcg ccg cac cag ccc ccc gcc tcc cgc tcc	325
177	Ala Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser	
178	35 40 45	
179	atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc	373
180	Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser	
181	50 55 60	
182	gtc gcc ctg ttc tat ttc aga ggc cag atg gat cct aat aga ata	421
183	Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
184	65 70 75	
185	tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa	469
186	Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu	
187	80 85 90 95	
188	aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta	517
189	Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu	
190	100 105 110	
191	ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg	565
192	Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val	
193	115 120 125	

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194	caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag	613
195	Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu	
196	130 135 140	
197	aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag	661
198	Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys	
199	145 150 155	
200	ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc	709
201	Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile	
202	160 165 170 175	
203	cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg	757
204	Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg	
205	180 185 190	
206	ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata	805
207	Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile	
208	195 200 205	
209	gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga	853
210	Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg	
211	210 215 220	
212	cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg	901
213	His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met	
214	225 230 235	
215	gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg	949
216	Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu	
217	240 245 250 255	
218	atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat	997
219	Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His	
220	260 265 270	
221	ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag	1045
222	Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu	
223	275 280 285	
224	gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag	1093
225	Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln	
226	290 295 300	
227	gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat	1135
228	Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp	
229	305 310 315	
230	tgagccccag tttttggagt gttatgtatt tcctggatgt ttggaaacat tttttaaaac	1195
231	aaggccaagaa agatgtataat aggtgtgtga gactactaag aggcattggcc ccaacgggtac	1255
232	acgactcagt atccatgctc ttgacccttg agagaacacg cgtatttaca gccagtggga	1315
233	gatgttagac tcatgggtgt ttacacaatg gttttaaat ttgtaatga attcctagaa	1375
234	ttaaaccaga ttggagcaat tacgggttga ccttatgaga aactgcattgt gggctatggg	1435
235	aggggttgttgc ccctgggtcat gtgcccccgttgc agagctgaag tggagagggt gtcattctagc	1495
236	gcaatttgaag gatcatctga aggggcaaat tcttttgaat tggttacatca tgctggacc	1555
237	tgcaaaaaat acttttcta atgaggagag aaaatatatg tattttata taatatctaa	1615
238	agttatattt cagatgtaat gtttcttg caaagtattt gaaattatatt ttgtgctata	1675
239	gtatggatt caaaatattt aaaaatgtct tgctgttgc atatattaatg ttttaatgt	1735
240	acagacatatt ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag	1795
241	ggggaaaaaaa tgttgttcc taatatcaaa tgcaagtatat ttcttcgttc ttttaatgtt	1855
242	aatagatttt ttcagacttg tcaagcctgt gcaaaaaat taaaatggat gccttgaataa	1915

VERIFICATION SUMMARY

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:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
:25 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
:166 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0
:653 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:0